```
        FILE 'CAPLUS' ENTERED AT 10:56:43 ON 23 FEB 2005
L1          114 S HIP1 OR (HUNTINGTON INTERACTING PROTEIN)
L2       631344 S CANCER? OR TUMOR? OR NEOPLAS?
L3           19 S L1 AND L2
L4        85732 S PROSTATE OR COLON
L5            4 S L4 AND L3
L6            0 S ROSS/AU
L7            1 S RAO/AU
L8            0 S MIZUKAMI/AU
L9            0 S L7 AND L5

        FILE 'CAPLUS' ENTERED AT 10:59:55 ON 23 FEB 2005

        FILE 'MEDLINE' ENTERED AT 11:00:02 ON 23 FEB 2005
L10         106 S HIP1 OR (HUNTINGTON INTERACTING PROTEIN)
L11     1688394 S CANCER? OR TUMOR? OR NEOPLAS?
L12          14 S L10 AND L11
L13           2 S L12 AND (PROSTATE OR COLON)

        FILE 'PCTFULL' ENTERED AT 11:01:12 ON 23 FEB 2005
L14          30 S HIP1 OR (HUNTINGTON INTERACTING PROTEIN)
L15       82521 S CANCER? OR TUMOR? OR NEOPLAS?
L16           1 S L14/TI
L17           3 S L14/AB
L18           3 S L14/CLM
L19           6 S L16 OR L17 OR L18
L20           6 S L19 AND L15
L21           2 S L20 AND (PROSTATE OR COLON)
```

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 18:00:49 ; Search time 561 Seconds
                                              (without alignments)
                                              6251.592 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 8122
Sequence: 1. ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10007047/runat_17022005_161809_3009/app_query.fasta_1.
4679
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10007047_@CGN_1_1_661_@runat_17022005_161809_3009 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_16Dec04:*
                  1: geneseqp1980s:*
                  2: geneseqp1990s:*
                  3: geneseqp2000s:*
                  4: geneseqp2001s:*
                  5: geneseqp2002s:*
                  6: geneseqp2003as:*
                  7: geneseqp2003bs:*
                  8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7422.5	91.4	1475	6	ABR63761	Abr63761 Human HIP
2	6415.5	79.0	1283	6	ABR63762	Abr63762 Human HIP
3	5035.5	62.0	1090	3	AAY59270	Aay59270 Human hun
4	4572	56.3	914	8	ADK60213	Adk60213 Angiogene
5	4572	56.3	914	8	ADK60514	Adk60514 Angiogene
6	4572	56.3	914	8	ADN01928	Adn01928 Human hun
7	4572	56.3	914	8	ADP73137	Adp73137 Angiogene
8	4572	56.3	914	8	ADP23863	Adp23863 PRO polyp
9	4556	56.1	914	2	AAW18030	Aaw18030 Huntingti
10	4556	56.1	914	3	AAY59269	Aay59269 Human hun
11	3210	39.5	756	3	AAY59272	Aay59272 Mouse hun
12	2564	31.6	1068	8	ABM81490	Abm81490 Tumour-as
13	2562.5	31.6	1068	3	AAY59273	Aay59273 Mouse hun
14	2016.5	24.8	890	6	AAE35345	Aae35345 Human col
15	1892	23.3	388	2	AAW18029	Aaw18029 Huntingti
16	1873	23.1	386	3	AAY59268	Aay59268 Human hun
17	1394.5	17.2	676	3	AAY59271	Aay59271 Human hun
18	1384.5	17.0	923	8	ADN23151	Adn23151 Bacterial
19	1219	15.0	1087	4	ABB65359	Abb65359 Drosophil
20	1219	15.0	1087	4	ABB65358	Abb65358 Drosophil
21	907.5	11.2	1077	8	ADN20979	Adn20979 Bacterial
22	789	9.7	282	4	AAB95632	Aab95632 Human pro
23	650	8.0	968	6	ABR53286	Abr53286 Protein s
24	650	8.0	968	7	ADK63576	Adk63576 Disease t
25	650	8.0	968	8	ADN19298	Adn19298 Bacterial
26	466.5	5.7	250	4	AAM25896	Aam25896 Human pro
27	427	5.3	2541	3	AAB41087	Aab41087 Human ORF
28	421	5.2	2541	7	ADP65318	Adp65318 Human tal
29	421	5.2	2541	8	ABM81037	Abm81037 Tumour-as
30	413	5.1	2541	5	ABB81459	Abb81459 Human Tal
31	413	5.1	2541	5	ADG90450	Adg90450 Human tal
32	413	5.1	2541	6	ABR47614	Abr47614 Breast ca
33	413	5.1	2541	7	ADD45522	Add45522 Human Pro
34	413	5.1	2541	7	ADE58868	Ade58868 Human Pro
35	413	5.1	2541	8	ADP85745	Adp85745 Human Tal
36	407	5.0	1177	4	AAM79794	Aam79794 Human pro
37	407	5.0	1177	4	AAM41079	Aam41079 Human pol
38	407	5.0	1177	4	AAM41098	Aam41098 Human pol
39	407	5.0	1933	8	ADQ19152	Adq19152 Human sof
40	407	5.0	2542	6	AAE33668	Aae33668 Human str
41	406	5.0	1134	4	AAM78810	Aam78810 Human pro
42	406	5.0	1144	4	AAM39293	Aam39293 Human pol
43	406	5.0	1165	4	AAM39312	Aam39312 Human pol
44	405	5.0	2541	7	ADE58866	Ade58866 Rat Prote
45	405	5.0	2541	7	ADD45520	Add45520 Rat Prote

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 18:12:35 ; Search time 113 Seconds
                                              (without alignments)
                                              5990.422 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 8122
Sequence: 1 ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: BLOSUM62
                   Xgapop 10.0 , Xgapext 0.5
                   Ygapop 10.0 , Ygapext 0.5
                   Fgapop 6.0 , Fgapext 7.0
                   Delop   6.0 , Delext   7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10007047/runat_17022005_161811_3039/app_query.fasta_1.
4679
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10007047_@CGN_1_1_120_@runat_17022005_161811_3039 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                   1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                   2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                   3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                   4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                   5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

```
                                    SUMMARIES
                         %
Result              Query
  No.    Score    Match Length DB   ID                        Description
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      1  5035.5   62.0   1090   3   US-09-085-199B-5          Sequence 5, Appli
      2  4556     56.1    914   3   US-09-085-199B-4          Sequence 4, Appli
      3  3210     39.5    756   3   US-09-085-199B-9          Sequence 9, Appli
      4  3034.5   37.4    601   4   US-09-949-016-10457       Sequence 10457, A
      5  2562.5   31.6   1068   3   US-09-085-199B-11         Sequence 11, Appl
      6  2016.5   24.8    890   4   US-09-849-602-19          Sequence 19, Appl
      7  1873     23.1    386   3   US-09-085-199B-2          Sequence 2, Appli
      8  1394.5   17.2    676   3   US-09-085-199B-7          Sequence 7, Appli
      9   394      4.9    333   4   US-09-248-796A-20655      Sequence 20655, A
     10   346      4.3   1972   4   US-08-875-435B-4          Sequence 4, Appli
     11   345.5    4.3   1857   4   US-09-917-254-91          Sequence 91, Appl
     12   345.5    4.3   1972   4   US-09-538-092-1084        Sequence 1084, Ap
     13   345.5    4.3   1984   4   US-09-949-016-7111        Sequence 7111, Ap
     14   345.5    4.3   1984   4   US-09-949-016-7112        Sequence 7112, Ap
     15   345.5    4.3   1984   4   US-09-949-016-7113        Sequence 7113, Ap
     16   343.5    4.2   1976   4   US-09-538-092-1078        Sequence 1078, Ap
     17   342      4.2    666   4   US-09-248-796A-20656      Sequence 20656, A
     18   332.5    4.1   1972   4   US-08-875-435B-3          Sequence 3, Appli
     19   315.5    3.9   2107   4   US-09-949-016-7646        Sequence 7646, Ap
     20   315.5    3.9   2107   4   US-09-949-016-7647        Sequence 7647, Ap
     21   308.5    3.8   2101   1   US-08-466-390-4           Sequence 4, Appli
     22   308.5    3.8   2101   1   US-08-470-950-4           Sequence 4, Appli
     23   308.5    3.8   2101   1   US-08-467-781-4           Sequence 4, Appli
     24   308.5    3.8   2101   1   US-08-195-487-4           Sequence 4, Appli
     25   308.5    3.8   2101   2   US-08-483-924-4           Sequence 4, Appli
     26   308.5    3.8   2101   3   US-09-452-294-1           Sequence 1, Appli
     27   308.5    3.8   2101   5   PCT-US93-06160-4          Sequence 4, Appli
     28   304.5    3.7   1960   4   US-09-538-092-1077        Sequence 1077, Ap
     29   304.5    3.7   1960   4   US-09-949-016-10872       Sequence 10872, A
     30   303.5    3.7   2482   1   US-08-328-254-6           Sequence 6, Appli
     31   303      3.7   3248   1   US-08-353-700-1           Sequence 1, Appli
     32   303      3.7   3248   5   PCT-US95-16216-1          Sequence 1, Appli
     33   302.5    3.7   3210   4   US-09-538-092-1154        Sequence 1154, Ap
     34   297      3.7   3878   4   US-09-914-259-11          Sequence 11, Appl
     35   294.5    3.6   2310   4   US-09-874-923-120         Sequence 120, App
     36   291.5    3.6   1427   4   US-09-538-092-1044        Sequence 1044, Ap
     37   290      3.6   3259   4   US-09-949-016-6507        Sequence 6507, Ap
     38   288.5    3.6    139   4   US-09-270-767-32557       Sequence 32557, A
     39   288.5    3.6   1362   4   US-09-949-016-7033        Sequence 7033, Ap
     40   288.5    3.6   1530   4   US-09-976-594-736         Sequence 736, App
     41   288.5    3.6   1530   4   US-09-949-016-6668        Sequence 6668, Ap
     42   288      3.5   2733   4   US-09-949-016-11433       Sequence 11433, A
     43   282      3.5   1938   4   US-09-949-016-6417        Sequence 6417, Ap
     44   282      3.5   2954   4   US-09-150-867-1           Sequence 1, Appli
     45   278      3.4   1940   4   US-09-538-092-901         Sequence 901, App
```

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 19:01:06 ; Search time 476 Seconds
                                              (without alignments)
                                              6234.079 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 8122
Sequence: 1 ccaagcttggtaccccggg..........gcatgcnntagagggcccta 4534

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 2760536

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10007047/runat_17022005_161812_3111/app_query.fasta_1.
4679
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10007047_@CGN_1_1_652_@runat_17022005_161812_3111
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_AA:*
                 1:   /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2:   /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 3:   /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 4:   /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5:   /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6:   /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7:   /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8:   /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9:   /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

```
11:   /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12:   /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13:   /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14:   /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15:   /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16:   /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17:   /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18:   /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19:   /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20:   /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	7422.5	91.4	1475	14	US-10-007-047-2	Sequence 2, Appli
	2	6415.5	79.0	1283	14	US-10-007-047-4	Sequence 4, Appli
	3	2016.5	24.8	890	10	US-09-849-602-19	Sequence 19, Appl
	4	1384.5	17.0	923	15	US-10-369-493-5804	Sequence 5804, Ap
	5	907.5	11.2	1077	15	US-10-369-493-3632	Sequence 3632, Ap
	6	650	8.0	968	15	US-10-369-493-1951	Sequence 1951, Ap
	7	466.5	5.7	250	15	US-10-296-115-1411	Sequence 1411, Ap
	8	413	5.1	2541	14	US-10-177-293-470	Sequence 470, App
	9	408	5.0	2545	15	US-10-092-900A-76	Sequence 76, Appl
	10	407	5.0	2542	17	US-10-479-764-2	Sequence 2, Appli
	11	397	4.9	949	16	US-10-408-765A-268	Sequence 268, App
	12	395	4.9	698	14	US-10-043-487-309	Sequence 309, App
	13	371.5	4.6	1879	15	US-10-296-115-1265	Sequence 1265, Ap
	14	345.5	4.3	1938	14	US-10-171-311-164	Sequence 164, App
	15	345.5	4.3	1945	10	US-09-927-597-2	Sequence 2, Appli
	16	345.5	4.3	1972	14	US-10-171-311-162	Sequence 162, App
	17	345.5	4.3	1972	15	US-10-341-434-103	Sequence 103, App
	18	345.5	4.3	1979	10	US-09-927-597-4	Sequence 4, Appli
	19	338	4.2	118	10	US-09-764-891-3307	Sequence 3307, Ap
	20	326.5	4.0	19723	15	US-10-084-846A-5	Sequence 5, Appli
	21	320.5	3.9	19695	15	US-10-084-846A-3	Sequence 3, Appli
	22	320	3.9	60	9	US-09-864-761-46124	Sequence 46124, A
c	23	320	3.9	639	16	US-10-408-765A-2802	Sequence 2802, Ap
	24	313.5	3.9	19662	15	US-10-084-846A-6	Sequence 6, Appli
	25	310	3.8	1959	15	US-10-028-248A-36	Sequence 36, Appl
	26	310	3.8	1959	15	US-10-107-782-36	Sequence 36, Appl
	27	309	3.8	1513	16	US-10-437-963-201466	Sequence 201466,
	28	308	3.8	1961	15	US-10-028-248A-103	Sequence 103, App
	29	308	3.8	1961	15	US-10-107-782-103	Sequence 103, App
	30	304.5	3.7	1960	15	US-10-236-031B-62	Sequence 62, Appl
	31	304.5	3.7	1960	15	US-10-028-248A-104	Sequence 104, App
	32	304.5	3.7	1960	15	US-10-107-782-104	Sequence 104, App
	33	303.5	3.7	19608	15	US-10-084-846A-8	Sequence 8, Appli
	34	302	3.7	1959	15	US-10-028-248A-106	Sequence 106, App
	35	302	3.7	1959	15	US-10-107-782-106	Sequence 106, App
c	36	299	3.6	19723	15	US-10-084-846A-5	Sequence 5, Appli
	37	298	3.7	860	15	US-10-080-334-166	Sequence 166, App

38	298	3.7	860	15	US-10-072-012-838	Sequence 838, App
39	298	3.7	860	15	US-10-037-417-59	Sequence 59, Appl
40	297.5	3.7	1178	14	US-10-128-714-8240	Sequence 8240, Ap
41	297.5	3.7	3899	14	US-10-171-311-4	Sequence 4, Appli
42	297.5	3.7	3907	14	US-10-171-311-2	Sequence 2, Appli
43	297.5	3.7	3917	14	US-10-171-311-8	Sequence 8, Appli
44	297.5	3.7	3925	14	US-10-171-311-6	Sequence 6, Appli
45	297	3.7	1017	16	US-10-408-765A-158	Sequence 158, App

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 18:04:24 ; Search time 142 Seconds
                                          (without alignments)
                                          6144.321 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 8122
Sequence: 1 ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10007047/runat_17022005_161810_3028/app_query.fasta_1.
4679
-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10007047_@CGN_1_1_225_@runat_17022005_161810_3028 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1384.5	17.0	923	2	S44664	ZK370.3 protein -
2	976.5	12.0	1054	2	T30177	cytoskeleton assem
3	883	10.9	1063	2	T18255	cytoskeleton assem
4	655	8.1	325	2	E88537	truncated ZK370.3
5	650	8.0	968	2	S63211	cytoskeleton assem
6	488	6.0	362	2	T20573	hypothetical prote
7	446	5.5	468	2	T43195	cytoskeleton assem
8	405	5.0	2541	2	S11661	talin - mouse
9	378	4.7	2491	2	A57036	talin - slime mold
10	346	4.3	1972	1	A41604	myosin heavy chain
11	343.5	4.2	1976	2	A59252	myosin heavy chain
12	334.5	4.1	1410	1	A57013	early endosome ant
13	332.5	4.1	1938	2	JC5421	smooth muscle myos
14	332.5	4.1	1972	2	JC5420	smooth muscle myos
15	327	4.0	1690	2	T13030	microtubule bindin
16	326.5	4.0	1979	1	S03166	myosin heavy chain
17	323.5	4.0	2007	1	B43402	myosin heavy chain
18	316.5	3.9	1992	2	A47297	myosin heavy chain
19	308.5	3.8	2101	2	A42184	nuclear mitotic ap
20	308	3.8	1961	1	A61231	myosin heavy chain
21	302	3.7	1959	1	A33977	myosin heavy chain
22	298	3.7	3187	2	JC5837	364K Golgi complex
23	297	3.7	1017	2	PC4035	cell-cycle-depende
24	294.5	3.6	1938	1	A40997	myosin heavy chain
25	293.5	3.6	848	2	A44972	paramyosin - nemat
26	293.5	3.6	1620	2	S61535	nucleotide-binding
27	293	3.6	1642	2	T08880	NMDA receptor-bind
28	292.5	3.6	725	2	A47168	cardiac morphogene
29	292	3.6	1927	2	A59236	embryonic muscle m
30	291.5	3.6	879	2	A48575	paramyosin - nemat
31	291.5	3.6	1175	2	D35815	myosin heavy chain
32	291.5	3.6	1201	2	B35815	myosin heavy chain
33	291.5	3.6	1427	2	S22695	restin - human
34	291	3.6	746	2	T47237	myosin II heavy ch
35	290.5	3.6	1957	2	T38077	hypothetical coile
36	290	3.6	3259	1	A56539	giantin - human
37	289.5	3.6	1475	2	T33318	hypothetical prote
38	288.5	3.6	1175	2	C35815	myosin heavy chain
39	288.5	3.6	1201	2	A35815	myosin heavy chain
40	288.5	3.6	2385	2	A32491	myosin heavy chain
41	288.5	3.6	2411	2	B32491	myosin heavy chain
42	288	3.5	1940	2	A59287	myosin heavy chain
43	288	3.5	3225	2	I52300	giantin - human
44	285.5	3.5	2442	2	T08621	centrosome associa
45	285	3.5	1269	2	F84730	probable myosin he

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 18, 2005, 18:01:24 ; Search time 714 Seconds
                                          (without alignments)
                                          6503.549 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 8122
Sequence: 1 ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US10007047/runat_17022005_161809_3017/app_query.fasta_1.
4679
-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10007047_@CGN_1_1_859_@runat_17022005_161809_3017 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result   Query

No.	Score	Match	Length	DB	ID	Description
1	5180	63.8	1030	1	HIP1_HUMAN	O00291 homo sapien
2	3998	49.2	906	2	Q8VD75	Q8vd75 mus musculu
3	2613.5	32.2	1066	2	Q6AZV5	Q6azv5 xenopus lae
4	2570	31.6	1068	2	Q6X276	Q6x276 oryctolagus
5	2569	31.6	1083	2	Q6ZQ77	Q6zq77 mus musculu
6	2564	31.6	1068	1	HIPR_HUMAN	O75146 homo sapien
7	2562.5	31.6	1068	1	HIPR_MOUSE	Q9jky5 mus musculu
8	2560	31.5	1079	2	Q99PW9	Q99pw9 rattus norv
9	2558.5	31.5	1068	2	Q6P1F5	Q6p1f5 mus musculu
10	2555.5	31.5	1068	2	Q9D689	Q9d689 mus musculu
11	2551.5	31.4	1008	2	Q6IRM8	Q6irm8 xenopus lae
12	1856	22.9	377	2	Q8C303	Q8c303 mus musculu
13	1600	19.7	973	2	Q7PMU0	Q7pmu0 anopheles g
14	1489.5	18.3	615	2	Q6NXG8	Q6nxg8 homo sapien
15	1402	17.3	682	2	Q80UP1	Q80up1 mus musculu
16	1392	17.1	927	1	SLA2_CAEEL	Q02328 caenorhabdi
17	1281	15.8	1124	2	Q8MQJ8	Q8mqj8 drosophila
18	1219	15.0	1087	2	Q86BS5	Q86bs5 drosophila
19	1078	13.3	423	2	Q8HXC4	Q8hxc4 macaca fasc
20	1045	12.9	230	2	Q8VHU1	Q8vhu1 rattus norv
21	986	12.1	1053	2	Q6CCQ4	Q6ccq4 yarrowia li
22	976.5	12.0	1054	2	O94097	O94097 yarrowia li
23	932.5	11.5	1053	2	Q7SDY1	Q7sdy1 neurospora
24	883	10.9	1063	2	O93959	O93959 candida alb
25	867.5	10.7	316	2	Q8BPA2	Q8bpa2 mus musculu
26	864.5	10.6	1092	1	SLA2_SCHPO	Q9p615 schizosacch
27	760.5	9.4	973	2	O74698	O74698 candida alb
28	723.5	8.9	949	2	Q6BIE3	Q6bie3 debaryomyce
29	648	8.0	968	1	SLA2_YEAST	P33338 saccharomyc
30	638.5	7.9	751	2	Q8MQK1	Q8mqk1 drosophila
31	615	7.6	952	2	Q6FP04	Q6fp04 candida gla
32	488	6.0	362	2	O62142	O62142 caenorhabdi
33	480.5	5.9	2614	2	O97054	O97054 dictyosteli
34	477.5	5.9	440	2	Q707Y5	Q707y5 pichia angu
35	421	5.2	2550	2	Q9UPX3	Q9upx3 homo sapien
36	416	5.1	2541	2	Q86YD0	Q86yd0 homo sapien
37	415.5	5.1	2541	2	Q8AWI0	Q8awi0 gallus gall
38	413	5.1	2541	1	TLN1_HUMAN	Q9y490 homo sapien
39	407	5.0	2542	1	TLN2_HUMAN	Q9y4g6 homo sapien
40	405	5.0	2541	1	TLN1_MOUSE	P26039 mus musculu
41	404	5.0	1452	2	Q8CDM9	Q8cdm9 mus musculu
42	401	4.9	2564	2	Q80TM2	Q80tm2 mus musculu
43	395	4.9	2717	2	Q7QJE3	Q7qje3 anopheles g
44	389.5	4.8	1775	2	Q68FD6	Q68fd6 mus musculu
45	383.5	4.7	671	2	Q6CUQ3	Q6cuq3 kluyveromyc

```
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OM nucleic - nucleic search, using sw model

Run on:          February 21, 2005, 01:06:15 ; Search time 18809 Seconds
                                              (without alignments)
                                 11680.363 Million cell updates/sec

Title:           US-10-007-047-1
Perfect score:   4534
Sequence:        1 ccaagcttggtaccccgggg..........gcatgcnntagagggcccta 4534

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:      9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  ·
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
                 14:  gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result             Query
  No.    Score   Match Length DB   ID                 Description
---------------------------------------------------------------------------
     1  3864.4    85.2   4707  6   CQ728008           CQ728008 Sequence
     2  3864.2    85.2   4714  9   HSU79734           U79734 Human hunti
     3  3859.6    85.1   6626  6   AX828392           AX828392 Sequence
```

	4	3754.8	82.8	4796	6	AR153626	AR153626 Sequence
	5	3754.8	82.8	4796	6	BD227037	BD227037 Apoptosis
	6	3088.2	68.1	3093	9	AF365404	AF365404 Homo sapi
	7	2364.6	52.2	6345	10	BC017516	BC017516 Mus muscu
	8	1664.4	36.7	2301	6	AR153628	AR153628 Sequence
	9	1664.4	36.7	2301	6	BD227039	BD227039 Apoptosis
	10	1163.4	25.7	1201	9	HSHIPIPRO	Y09420 H.sapiens m
	11	1155.2	25.5	1164	6	AR153625	AR153625 Sequence
	12	1155.2	25.5	1164	6	BD227036	BD227036 Apoptosis
	13	1118.4	24.7	3715	6	AR153661	AR153661 Sequence
	14	1118.4	24.7	3715	6	BD227072	BD227072 Apoptosis
	15	1118.4	24.7	3715	9	HSAHIPI28	AF052288 Homo sapi
	16	1116.8	24.6	134979	9	AC018720	AC018720 Homo sapi
c	17	1110.6	24.5	180399	2	AC079252	AC079252 Homo sapi
c	18	1090.6	24.1	183915	2	AC073967	AC073967 Homo sapi
c	19	1088.8	24.0	171329	2	AC147785	AC147785 Pan trogl
c	20	1085.2	23.9	172105	9	AC093135	AC093135 Pan trogl
c	21	1085.2	23.9	199670	9	AC142303	AC142303 Pan trogl
c	22	1085.2	23.9	221091	9	AC146228	AC146228 Pan trogl
	23	973.2	21.5	4412	10	BC065101	BC065101 Mus muscu
	24	971.6	21.4	4332	10	AK129182	AK129182 Mus muscu
	25	970	21.4	3210	10	AF221713	AF221713 Mus muscu
	26	970	21.4	3979	6	AR153629	AR153629 Sequence
	27	970	21.4	3979	6	BD227040	BD227040 Apoptosis
	28	961.8	21.2	4165	5	AJ720293	AJ720293 Gallus ga
c	29	955.8	21.1	157502	2	AC145842	AC145842 Papio anu
c	30	955.8	21.1	192030	9	AC092406	AC092406 Papio anu
	31	951.4	21.0	3207	4	AY260906	AY260906 Oryctolag
	32	942.2	20.8	4293	10	AB005052	AB005052 Rattus no
	33	926.4	20.4	4457	6	CQ861626	CQ861626 Sequence
	34	926.4	20.4	4457	9	AB014555	AB014555 Homo sapi
	35	861.2	19.0	3186	6	CQ725683	CQ725683 Sequence
	36	838.2	18.5	4067	5	BC077182	BC077182 Xenopus l
	37	815.6	18.0	4508	6	AX781120	AX781120 Sequence
	38	802.2	17.7	3190	5	BC070829	BC070829 Xenopus l
	39	758.8	16.7	3726	10	BC036288	BC036288 Mus muscu
	40	715.4	15.8	3876	9	AB013384	AB013384 Homo sapi
	41	695.8	15.3	1365	5	CR733418	CR733418 Gallus ga
c	42	640.8	14.1	71103	2	AC026507	AC026507 Homo sapi
	43	563.4	12.4	601	6	AX321326	AX321326 Sequence
	44	560.6	12.4	2009	9	BC067085	BC067085 Homo sapi
	45	557.8	12.3	814	10	AF388529	AF388529 Rattus no

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 00:54:00 ; Search time 2200 Seconds
                                              (without alignments)
                                              12200.049 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 4534
Sequence: 1 ccaagcttggtaccccggg.........gcatgcnntagagggcccta 4534

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   4532 100.0   4534   10   ACC85533   Acc85533 Human HIP
     2   3911   86.3   3911   10   ACC85534   Acc85534 Human HIP
     3   3869   85.3   6624   13   ADQ86162   Adq86162 Human tum
     4   3867   85.3   6623   13   ACN38651   Acn38651 Tumour-as

	5	3859.6	85.1	6626	12	ADK60463	Adk60463 Angiogene
	6	3859.6	85.1	6626	12	ADK60764	Adk60764 Angiogene
	7	3859.6	85.1	6626	12	ADN01766	Adn01766 Human hun
	8	3859.6	85.1	6626	12	ADP73086	Adp73086 Angiogene
	9	3859.6	85.1	6626	13	ADP23862	Adp23862 PRO polyp
	10	3754.8	82.8	4796	2	AAT67187	Aat67187 Huntingti
	11	3750	82.7	4796	3	AAZ58746	Aaz58746 Human hun
	12	1662.8	36.7	2301	3	AAZ58748	Aaz58748 Mouse hun
	13	1155.2	25.5	1164	2	AAT67186	Aat67186 Huntingti
	14	1155.2	25.5	1164	3	AAZ58745	Aaz58745 Human hun
	15	1118.4	24.7	3715	3	AAZ58781	Aaz58781 Human HIP
	16	1116.8	24.6	65454	12	ADN01773	Adn01773 Human hun
	17	970	21.4	3979	3	AAZ58749	Aaz58749 Mouse hun
	18	926.4	20.4	4457	13	ADR52908	Adr52908 Drug ther
	19	924.8	20.4	4461	13	ACN39595	Acn39595 Tumour-as
	20	815.6	18.0	4508	10	ADF82721	Adf82721 Leukaemia
	21	715.4	15.8	3876	10	AAD54024	Aad54024 Human col
	22	563.4	12.4	601	6	AAS61792	Aas61792 Lung smal
	23	483.2	10.7	3251	3	AAZ58747	Aaz58747 Human hun
c	24	415.8	9.2	482	10	ADD32881	Add32881 Human mit
c	25	394.4	8.7	5853	12	ADK60309	Adk60309 Angiogene
c	26	394.4	8.7	5853	12	ADK60610	Adk60610 Angiogene
c	27	394.4	8.7	5853	12	ADP73233	Adp73233 Angiogene
c	28	393	8.7	393	12	ADK60263	Adk60263 Antisense
c	29	393	8.7	393	12	ADK60564	Adk60564 Antisense
c	30	393	8.7	393	12	ADP73187	Adp73187 Angiogene
	31	369.8	8.2	2106	4	AAH18339	Aah18339 Human cDN
	32	354	7.8	561	13	ADQ53538	Adq53538 Novel can
	33	341	7.5	746	4	AAH08699	Aah08699 Human cDN
	34	331	7.3	331	6	AAS61782	Aas61782 Lung smal
	35	302.6	6.7	518	4	AAI42717	Aai42717 Probe #11
	36	302.6	6.7	518	4	AAK36916	Aak36916 Human bon
	37	302.6	6.7	518	4	AAK11093	Aak11093 Human bra
	38	302.6	6.7	518	4	ABS36587	Abs36587 Human liv
	39	302.6	6.7	518	6	ABS10924	Abs10924 Human gen
	40	236	5.2	484	9	ACH40550	Ach40550 Human foe
	41	197.4	4.4	404	10	ACC85536	Acc85536 Human HIP
	42	187	4.1	436	3	AAZ58765	Aaz58765 Human hun
	43	186.2	4.1	3911	4	ABL17083	Abl17083 Drosophil
	44	186.2	4.1	4115	4	ABL17085	Abl17085 Drosophil
	45	184	4.1	184	4	AAI55778	Aai55778 Probe #24

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 08:18:12 ; Search time 2330 Seconds
                                          (without alignments)
                                          11501.369 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 4534
Sequence: 1 ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
                 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4532	100.0	4534	15	US-10-007-047-1	Sequence 1, Appli
	2	4532	100.0	4534	18	US-10-767-325-1	Sequence 1, Appli
	3	3911	86.3	3911	15	US-10-007-047-3	Sequence 3, Appli
	4	3911	86.3	3911	18	US-10-767-325-3	Sequence 3, Appli
	5	3859.6	85.1	6626	17	US-10-293-864-4	Sequence 4, Appli
	6	1116.8	24.6	65454	17	US-10-293-864-11	Sequence 11, Appl
	7	926.4	20.4	4457	18	US-10-775-169-259	Sequence 259, App
	8	715.4	15.8	3876	10	US-09-849-602-4	Sequence 4, Appli
	9	563.4	12.4	601	9	US-09-833-790-343	Sequence 343, App
	10	331	7.3	331	9	US-09-833-790-333	Sequence 333, App
	11	302.6	6.7	518	9	US-09-864-761-13307	Sequence 13307, A
	12	236	5.2	484	10	US-09-918-995-27762	Sequence 27762, A
	13	197.4	4.4	404	15	US-10-007-047-6	Sequence 6, Appli
	14	197.4	4.4	404	18	US-10-767-325-6	Sequence 6, Appli
	15	184	4.1	184	9	US-09-864-761-29870	Sequence 29870, A
	16	181.6	4.0	1038	17	US-10-296-115-672	Sequence 672, App
	17	169.6	3.7	469	10	US-09-918-995-28069	Sequence 28069, A
	18	155.6	3.4	357	10	US-09-764-891-620	Sequence 620, App
	19	144.6	3.2	577	9	US-09-864-761-8117	Sequence 8117, Ap
	20	141	3.1	141	9	US-09-864-761-24860	Sequence 24860, A
	21	141	3.1	2080	17	US-10-108-260A-387	Sequence 387, App
c	22	126.6	2.8	161	16	US-10-029-386-16651	Sequence 16651, A
c	23	126.6	2.8	564	16	US-10-029-386-2951	Sequence 2951, Ap
	24	126.4	2.8	3231	17	US-10-369-493-27319	Sequence 27319, A
	25	117.6	2.6	1835	13	US-10-012-690-1	Sequence 1, Appli
	26	104	2.3	675	18	US-10-653-047-4385	Sequence 4385, Ap
	27	102	2.2	556	18	US-10-653-047-590	Sequence 590, App
	28	91.8	2.0	1315	17	US-10-264-049-806	Sequence 806, App
	29	90.8	2.0	2076	9	US-09-822-830A-386	Sequence 386, App
	30	90.8	2.0	2098	14	US-10-043-487-108	Sequence 108, App
	31	90.8	2.0	7995	9	US-09-864-864-333	Sequence 333, App
	32	90.8	2.0	8078	9	US-09-791-942-3	Sequence 3, Appli
	33	90.8	2.0	8078	15	US-10-177-293-469	Sequence 469, App
	34	90.8	2.0	8078	18	US-10-415-463-3	Sequence 3, Appli
	35	90.8	2.0	8187	17	US-10-131-827-8866	Sequence 8866, Ap
	36	90.8	2.0	8648	14	US-10-198-846-9840	Sequence 9840, Ap
	37	90.8	2.0	8791	18	US-10-719-993-102	Sequence 102, App
	38	90.8	2.0	8791	18	US-10-719-993-103	Sequence 103, App
c	39	90.8	2.0	21295	16	US-10-252-157-467	Sequence 467, App
c	40	88.8	2.0	597	13	US-10-027-632-270825	Sequence 270825,
c	41	88.8	2.0	597	17	US-10-027-632-270825	Sequence 270825,
	42	80.8	1.8	458	10	US-09-918-995-28705	Sequence 28705, A
	43	79.8	1.8	3489	11	US-09-894-273-1	Sequence 1, Appli
	44	79.8	1.8	3489	15	US-10-294-804-1	Sequence 1, Appli
	45	79.8	1.8	3489	18	US-10-194-046-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2005, 02:11:36 ; Search time 13445 Seconds
                                             (without alignments)
                                 12836.251 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 4534
Sequence: 1 ccaagcttggtacccccggg..........gcatgcnntagagggcccta 4534

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   1001.2   22.1   3403 3 AK087586   AK087586 Mus muscu
     2   973.2   21.5   4001 3 AK014542   AK014542 Mus muscu
     3   962.2   21.2   4285 3 BC062914   BC062914 Mus muscu
     4   900.8   19.9   1113 4 BM556334   BM556334 AGENCOURT
     5   900.6   19.9   1041 4 BM550560   BM550560 AGENCOURT
     6   899.8   19.8   939 5 BQ951181   BQ951181 AGENCOURT
     7   836   18.4   920 6 CA976174   CA976174 AGENCOURT
     8   833.6   18.4   912 5 BQ651977   BQ651977 AGENCOURT

	9	831.4	18.3	896	5	BU169905	BU169905	AGENCOURT
	10	810.8	17.9	867	6	CD251809	CD251809	AGENCOURT
	11	797.2	17.6	1164	4	BM556298	BM556298	AGENCOURT
	12	780.4	17.2	968	5	BQ643973	BQ643973	AGENCOURT
	13	747.4	16.5	854	4	BI826617	BI826617	603077068
	14	705.8	15.6	740	4	BI832375	BI832375	603072967
c	15	705.4	15.6	861	7	CK776278	CK776278	967424 MA
	16	676.4	14.9	690	7	CN387640	CN387640	170004551
	17	674.8	14.9	808	4	BI460519	BI460519	603201132
	18	671.6	14.8	3138	9	AY416115	AY416115	Homo sapi
	19	671.2	14.8	1090	5	BM916156	BM916156	AGENCOURT
	20	666.2	14.7	1174	4	BM809694	BM809694	AGENCOURT
	21	662.6	14.6	1232	5	BM911401	BM911401	AGENCOURT
	22	662	14.6	1076	4	BM562169	BM562169	AGENCOURT
	23	658	14.5	3079	9	AY416117	AY416117	Mus muscu
	24	649.2	14.3	918	4	BI520505	BI520505	603071510
	25	646	14.2	919	4	BM465156	BM465156	AGENCOURT
c	26	634.8	14.0	864	7	CK463860	CK463860	934794 MA
	27	630.6	13.9	901	5	BU151859	BU151859	AGENCOURT
	28	628.6	13.9	804	4	BI561631	BI561631	603256046
	29	622	13.7	649	7	CN387638	CN387638	170005328
	30	606.2	13.4	755	5	BQ951163	BQ951163	AGENCOURT
	31	595	13.1	982	4	BM009576	BM009576	603630147
	32	586.8	12.9	592	5	BP282107	BP282107	BP282107
	33	559.8	12.3	829	4	BG027957	BG027957	602294559
	34	545.2	12.0	1034	4	BM560226	BM560226	AGENCOURT
	35	537.8	11.9	638	5	BU706443	BU706443	UI-M-FO0-
	36	522.6	11.5	914	6	CB195314	CB195314	AGENCOURT
	37	518.6	11.4	525	7	CN387642	CN387642	170004245
	38	518.2	11.4	705	6	CA750285	CA750285	UI-M-FD0-
	39	514	11.3	662	2	BB865663	BB865663	BB865663
	40	513.6	11.3	640	2	BB866223	BB866223	BB866223
	41	507.2	11.2	3114	9	AY416116	AY416116	Pan trogl
	42	502	11.1	672	2	BB865439	BB865439	BB865439
	43	501.2	11.1	602	6	CD542105	CD542105	B0237G02-
	44	496.4	10.9	639	2	BB665816	BB665816	BB665816
	45	491.8	10.8	495	1	AA402004	AA402004	zt62f10.r